

IUBMB Enzyme Nomenclature

EC 3.4.11.10

Common name: bacterial leucyl aminopeptidase

Reaction: Release of an N-terminal amino acid, preferentially leucine, but not glutamic or aspartic acids

Other names: *Aeromonas proteolytica* aminopeptidase

Comments: A zinc enzyme. Forms of the enzyme have been isolated from *Aeromonas proteolytica*, *E. coli* and *Staphylococcus thermophilus*. Examples are known from peptidase families M17 and M28 (of leucyl aminopeptidase and aminopeptidase Y, respectively)

Links to other databases: [BRENDA](#), [EXPASY](#), [MEROPS](#), CAS registry number: 37288-67-8

References

1. Prescott, J.M. and Wilkes, S.H. *Aeromonas* aminopeptidase: purification and some general properties. *Arch. Biochem. Biophys.* 117 (1966) 328-336. [Medline UI: [67183850](#)]
2. Dick, A.J., Matheson, A.T. and Wang, J.H. A ribosomal-bound aminopeptidase in *Escherichia coli* B: purification and properties. *Can. J. Biochem.* 48 (1970) 1181-1188. [Medline UI: [71025351](#)]
3. Rabier, D. and Desmazeaud, M.J. Inventaire des différentes activités peptidiques intracellulaires de *Streptococcus thermophilus*. Purification et propriétés d'une dipeptide-hydrolase et d'une aminopeptidase. *Biochimie (Paris)* 55 (1973) 389-404. [Medline UI: [74024326](#)]

[EC 3.4.11.10 created 1972]

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Arch. Biochem. Biophys. 1966;117:328-336

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Aeromonas aminopeptidas : purification and some general properties

Prescott, J.M.; Wilkes, S.H.; c

Legend: valid for all references of this EC number; valid only for this reference; valid for all references of this EC Number but only for described organisms (see field "Organism")

Organism Aeromonas proteolytica

See also following references to EC number 3.4.11.10 (sorted by authors):

1. Baker *et al.*(1985); 6. Baker *et al.*(1983); 17. Bennett *et al.*(1997); 18. Chevrier *et al.*(1996); 19. De Paola *et al.*(1999); 23. Dick *et al.*(1970); 21. Huntington *et al.*(1999); 22. Izawa *et al.*(1997); 8. Kettner *et al.*(1974); 9. Kettner *et al.*(1974); 13. Maekinen *et al.*(1982); 14. Maekinen *et al.*(1982); 3. Prescott *et al.*(1985); 5. Prescott *et al.*(1983); 7. Prescott *et al.*(1975); 12. Prescott *et al.*(1966); 11. Prescott *et al.*(1971); 16. Schalk *et al.*(1992); 20. Ustynyuk *et al.*(1999); 10. Wagner *et al.*(1972); 15. Wilkes *et al.*(1973); 2. Wilkes *et al.*(1985); 4. Wilkes *et al.*(1983);

Recommended Name bacterial leucyl aminopeptidase

EC Number 3.4.11.10

CAS Registry Number 37288-67-8

Reaction protein + H₂O = amino acid + protein



Substrates/Products

(S:=Substrates, CS:=Commentary Substrate, LS:=Literature Substrate, OS:=Organism Substrate, P:=Product, CP:=Commentary Product, LP:=Literature Product, OR:=Organism, OP:=Organism Product, RE:=Reversibility)

Aeromonas proteolytica:

S= Leu-beta-naphthylamide + H₂O, LS= 7,12, OS= Aeromonas proteolytica, P= Leu + beta-naphthylamine, LP= 7,12, OR= Aeromonas proteolytica,

S= Leu-Tyr + H₂O, LS= 7,10,12, OS= Aeromonas proteolytica, P= Leu + Tyr, LP= 7,10,12, OR= Aeromonas proteolytica,

S= Leu-Gly + H₂O, LS= 12, OS= Aeromonas proteolytica, P= Leu + Gly, LP= 12, OR= Aeromonas proteolytica,

S= Val-Gly + H₂O, LS= 12, OS= Aeromonas proteolytica, P= Val + Gly, LP= 12, OR= Aeromonas proteolytica,

S= Ala-Gly + H₂O, LS= 12, OS= Aeromonas proteolytica, P= Ala + Gly, LP= 12, OR= Aeromonas proteolytica,

S= Tyr-Gly + H₂O, LS= 12, OS= Aeromonas proteolytica, P= Tyr + Gly, LP= 12, OR= Aeromonas proteolytica,

S= Phe-Gly + H₂O, LS= 12, OS= Aeromonas proteolytica, P= Phe + Gly, LP= 12, OR= Aeromonas proteolytica,

S= Lys-Gly + H₂O, LS= 12, OS= Aeromonas proteolytica, P= Lys + Gly, LP= 12, OR= Aeromonas proteolytica,

S= DL-Leu-Gly-DL-Phe + H₂O, LS= 12, OS= Aeromonas proteolytica, P= DL-Leu + Gly-DL-Phe, LP= 12, OR= Aeromonas proteolytica,

S= DL-Ala-Gly-Gly + H₂O, LS= 12, OS= Aeromonas proteolytica, P= DL-Ala + Gly-Gly, LP= 12, OR= Aeromonas proteolytica,

S= DL-Leu-Gly-Gly + H₂O, LS= 12, OS= Aeromonas proteolytica, P= DL-Leu + Gly-Gly, LP= 12, OR= Aeromonas proteolytica,

S = Phe-beta-naphthylamide + H₂O, CS= 18% of rate of hydrolysis of Leu-beta-naphthylamide (see ref.: this reference) , LS= 12, OS= *Aeromonas proteolytica*, P= Phe + beta-naphthylamine, LP= 12, OR= *Aeromonas proteolytica*,

S = Thr-beta-naphthylamide + H₂O, CS= 3.3% of rate of hydrolysis of Leu-beta-naphthylamide (see ref.: this reference) , LS= 12, OS= *Aeromonas proteolytica*, P= Thr + beta-naphthylamine, LP= 12, OR= *Aeromonas proteolytica*,

Natural Substrates/Natural Products:

(S:=Natural Substrates, CS:=Commentary Natural Substrate, LS:=Literature Natural Substrate, OS:=Organism Substrate, P:=Natural Product, CP:=Commentary Natural Product, LP:=Literature Natural Product, OR:=Organism, OP:=Organism Natural Product, RE:=Reversibility)

Aeromonas proteolytica:

S = peptides + H₂O, LS= 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21, OS= *Aeromonas proteolytica*, OP= ir <22>

Inhibitors:

(IN:=Inhibitors, CO:=Commentary)

Aeromonas proteolytica:

IN= cysteine, CO= 60% loss of activity at 10 mM (see ref.: this reference)

IN= EDTA,

IN= Na₂S, CO= 60% loss of activity at 10 mM (see ref.: this reference)

IN= thioglycollate, CO= 60% loss of activity at 10 mM (see ref.: this reference)

Localization:

(LO:=Localization, CO:=Commentary)

Aeromonas proteolytica:

LO= extracellular,

Molecular Weight:

(MW:=Molecular Weight [Da], MWM:=Molecular Weight Maximum [Da], CO:=Commentary)

Aeromonas proteolytica:

MW= 29500, CO= sedimentation velocity (see ref.: 7, 11, this reference)

Metals/Ions:

(MI:=Metal Ions, CO:=Commentary)

Aeromonas proteolytica:

MI= Zn²⁺, CO= bound zinc ion interacts directly with substrate during catalysis but not during substrate binding, contains 2 mol zinc per mol enzyme but only one site has to be occupied in order to facilitate catalysis (see ref.: 1) ; zinc can be replaced by other metals, nonidentical, interacting metal-binding sites, magnetic circular dichroism study, hyperactivation by sequential addition of metal ions, sequence of addition effects activity (see ref.: 3) ; if copper or cobalt are added prior to zinc in sequential substitution experiments, activation is two orders of magnitude higher than in the opposite sequence, which suggests two metal-binding sites with different functions (see ref.: 5) ; 2 mol zinc per mol enzyme (see ref.: 11) ; no loss of zinc upon photoactivation (see ref.: 14)

MI= Co²⁺, CO= can replace zinc, nonidentical, interacting metal-binding sites, magnetic circular dichroism study, hyperactivation by sequential addition of different metal ions, sequence of addition effects activity (see ref.: 3) ; if copper or cobalt are added prior to zinc in sequential substitution experiments, activation is two orders of magnitude higher than the other way round, which suggests two metal-binding sites with different functions (see ref.: 5) ; 65% of activity of zinc enzyme (see ref.: this reference) ; spectroscopically distinct cobalt sites in heterodimetallic enzymes, implications for substrate binding (see ref.: 17)

MI= Mn²⁺, CO= 58% of activity of zinc enzyme (see ref.: this reference)

Purification:

Aeromonas proteolytica:

⇒ based on t-butyloxycarbonyl-L-Leu-bromomethyl ketone affinity chromatography (see ref.: 9) ; revised procedure (see ref.: 11) ; 2 new procedures (see ref.: 16)

Specific Activity:

(SA:=Specific Activity [micromol/min/mg], SM:=Specific Activity Maximum, CO:=Commentary)

Aeromonas proteolytica:

SA= 21,

T_{mp} rature Stability:

(TS:=Temperature stability[°C], TM:=Temperature stability maximum[°C], CO:=Commentary)

Aeromonas proteolytica:

TS= 70, CO= below, but tolerates exposure up to a few hours (see ref.: 7, this reference)

pH Optimum:

(pH:=pH Optimum, pM:=pH Optimum Maximum, CO:=Commentary)

Aeromonas proteolytica:

pH= 8.5,

pH Stability:

(pS:=pH Stability, pM:=pH Stability Maximum, CO:=Commentary)

Aeromonas proteolytica:

pS= 5.5, pM= 8.5, CO= above 40% maximal activity across range (see ref.: this reference)

PDB ID Number:

(PDB ID Number/Organism)

1AMP/ Vibrio proteolyticus | 1CP6/ Aeromonas proteolytica | 1FT7/ Aeromonas proteolytica | 1IGB/ Vibrio proteolyticus | 1LOK/

Aeromonas proteolytica | 1XJO/ Streptomyces griseus
